

<110> KAO CORPORATION

<130> KS0795

<151> 2003. 11. 7

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〈213〉 Bacillus sp. KSM-S237

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gaaataaaag tagaagacaa aggacataag aaaattgcat tagttttaat tatagaaaac 180

gcctttttat aattatttat acctagaacg aaaataactgt ttcgaaagcg gtttactata 240

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gtaagcgggtt aaccttgtgc tatatgccga tttaggaagg ggggtagatt gagtcaagta 420

gtaataatat agataactta taagttgttg agaagcagga gagcatctgg gttactcaca 480

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Lys Gln Leu Ile Ser Ser Ile Leu Ile Leu Val Leu Leu Leu Ser Leu
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Lys His Leu Leu Gly Asn Asp Asn Val Lys Arg Pro Ser Glu Ala Gly
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Ala Leu Gln Leu Gln Glu Val Asp Gly Gln Met Thr Leu Val Asp Gln
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cat gga gaa aaa att caa tta cgt gga atg agt aca cac gga tta cag His Gly Glu Lys Ile Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln 45 50 55	833
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 Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp
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 Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
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330

335

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Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu	
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gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg gtt cgc ggt Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly 610 615 620 625	2571
gaa aat gat tat gta act ttt gat ttc tat cta gat cca gtt cgt gca Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala 630 635 640	2619
aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn 645 650 655	2667
ggg tat lgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu 660 665 670	2715
tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys 675 680 685	2763
att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg 690 695 700 705	2811
aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg 710 715 720	2859
gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro 725 730 735	2907
gtt gaa cca gag cca gtt gat cct ggc gaa gag acg ccg cct gtc gat Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp 740 745 750	2955
gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys 755 760 765	3003
gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala 770 775 780 785	3051
atc aaa aat gag gct acg aaa aaa taatctaala aactagllat agggttatct	3105

Ile Lys Asn Glu Ala Thr Lys Lys
790

aaaggtctga tgcagatctt ttagataacc tttttttgca taactggaca tagaatggtt 3165
attaaagaaa gcaaggtgtt tatacgatat taaaaaggta gcgattttta attgaaacct 3225
ttaataatgt cttgtgatag aatgatgaag taatttaaga gggggaaacg aagtgaaaac 3285
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<213> Bacillus sp. KSM-64

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-10 -5 -1 1

Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val
5 10 15

Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly
20 25 30 35

Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly
40 45 50

Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn
55 60 65

Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile Arg Leu
70 75 80

Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu Leu Ile
85 90 95

Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn Asp Met
100 105 110 115

Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp
120 125 130

Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile Ala Ala Leu
135 140 145

Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser
150 155 160

Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp
165 170 175

Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Asp
180 185 190 195

Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp
 200 205 210
 Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
 215 220 225
 Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr
 230 235 240
 Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met
 245 250 255
 Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr
 260 265 270 275
 Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro Tyr Phe Asp
 280 285 290
 Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp
 295 300 305
 Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr
 310 315 320
 Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp Pro Gly Pro
 325 330 335
 Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val
 340 345 350 355
 Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys
 360 365 370
 Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe
 375 380 385
 Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile Glu Asn Glu
 390 395 400
 Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn Asp Val Ser
 405 410 415
 Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp Gly Trp Gly
 420 425 430 435
 Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val Ile
 440 445 450
 Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro Gln Gly Pro
 455 460 465
 Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val Glu Pro Thr
 470 475 480

Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu Thr Ile Thr
 485 490 495
 Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His Ala Glu Asn
 500 505 510 515
 Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu Gly Ala Asp
 520 525 530
 Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val Glu Ile
 535 540 545
 Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser Val Phe
 550 555 560
 Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val
 565 570 575
 Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala Leu Ser
 580 585 590 595
 Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp Ala Thr
 600 605 610
 Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly Glu Asn
 615 620 625
 Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu
 630 635 640
 Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn Gly Tyr
 645 650 655
 Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu
 660 665 670 675
 Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn
 680 685 690
 Val Arg Asp Ile Thr Asn Ile Gln Asp Thr Leu Leu Arg Asn Met
 695 700 705
 Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg Val Phe
 710 715 720
 Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu
 725 730 735
 Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys
 740 745 750 755
 Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala
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Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala Ile Lys
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Asn Glu Ala Thr Lys Lys
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 aactaaagat tgaaatagaa gtagaagaca acggacataa gaaaattgta ttagttttta
 180
 ttatagaaaa cgcttttcta taattattta tacctagaac gaaaatactg tttcgaaagc
 240
 ggtttactat aaaaccttat attccggctc ttttttttaa caggggggtga aaattcactc
 300
 tagtattcta atttcaacat gctataataa atttgtaaga cgcaatatac atcttttttt
 360
 tatgatattt gtaagcggit aaccttgtgc tatatgccga tttaggaagg gggtagattg
 420
 agtcaagtag tcataattta gataacttat aagtgtgtga gaagcaggag agaatciggg
 480
 ttactcacia gtttttttaa acattatcga aagcactttc ggttatgctt atgaatttag
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 ctatttgatt caattacttt aataatttta ggaggtaat atg atg tta aga aag
 594
 Met Met Leu Arg Lys
 -15

aaa aca aag cag tlg ggt cga cca gca caa gcc gat gga tlg aac ggt
 642
 Lys Thr Lys Gln Leu Gly Arg Pro Ala Gln Ala Asp Gly Leu Asn Gly
 -10 -5 -1 1 5

acg atg atg cag tat tat gag tgg cat ttg gaa aac gac ggg cag cat
 690
 Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp Gly Gln His
 10 15 20

tgg aat cgg ttg cac gat gat gcc gca gct ttg agt gat gct ggt att
 738
 Trp Asn Arg Leu His Asp Asp Ala Ala Leu Ser Asp Ala Gly Ile
 25 30 35

aca gct att tgg att ccg cca gcc tac aaa ggt aat agt cag gcg gat
 786
 Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser Gln Ala Asp
 40 45 50

gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag ttc aat caa
 834
 Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln
 55 60 65

aag ggt act gtt cga acg aaa tac gga act aag gca cag ctt gaa cga
 882
 Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln Leu Glu Arg

70	75	80	85	
gct att ggg tcc ctt aaa tct aat gat atc aat gta tac gga gat gtc Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn Val Tyr Gly Asp Val 90 95 100				930
gtg atg aat cat aaa atg gga gct gat ttt acg gag gca gtg caa gct Val Met Asn His Lys Met Gly Ala Asp Phe Thr Glu Ala Val Gln Ala 105 110 115				978
gtt caa gla aat cca acg aat cgt tgg cag gat att tca ggt gcc lac Val Gln Val Asn Pro Thr Asn Arg Trp Glu Asp Ile Ser Gly Ala Tyr 120 125 130				1026
acg att gat gcg tgg acg ggt ttc gac ttt tca ggg cgt aac aac gcc Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser Gly Arg Asn Asn Ala 135 140 145				1074
tat tca gat ttt aag tgg aga tgg ttc cat ttt aat ggt gtt gac tgg Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe Asn Gly Val Asp Trp 150 155 160 165				1122
gat cag cgc tat caa gaa aat cat att ttc cgc ttt gca aat acg aac Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg Phe Ala Asn Thr Asn 170 175 180				1170
tgg aac tgg cga gtg gat gaa gag aac ggt aat tat gat tac ctg tta Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn Tyr Asp Tyr Leu Leu 185 190 195				1218
gga tgg aat atc gac ttt agt cat cca gaa gla caa gat gag ttg aag Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val Gln Asp Glu Leu Lys 200 205 210				1266
gat tgg ggt agc tgg ttt acc gat gag tta gat ttg gat ggt tat cgt Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp Leu Asp Gly Tyr Arg 215 220 225				1314
tta gat gct att aaa cat att cca ttc tgg tat aca tct gat tgg gtt Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr Thr Ser Asp Trp Val 230 235 240 245				1362
cgg cat cag cgc aac gaa gca gat caa gat tta ttt gtc gla ggg gaa Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu Phe Val Val Gly Gln 250 255 260				1410
tat tgg aag gat gac gla ggt gct ctc gaa ttt tat tta gat gaa atg Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe Tyr Leu Asp Glu Met 265 270 275				1458
aal tgg gag atg tct cta ttc gat gti cca ctt aat tat aat ttt tac Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu Asn Tyr Asn Phe Tyr 280 285 290				1506
cgg gct tca caa cna ggt gga agc tat gat atg cgt aat att tta cga Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met Arg Asn Ile Leu Arg 295 300 305				1554
gga tct tta gla gaa gcg cat ccg atg cat gca gti acg ttt gti gat Gly Ser Leu Val Glu Ala His Pro Met His Ala Val Thr Phe Val Asp 310 315 320 325				1602
aat cat gat act cag cca ggg gag tca tta gag tca tgg gti gct gat Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu Ser Trp Val Ala Asp 330 335 340				1650
tgg ttt aag cca ctt gct tat gcg aca att ttg acg cgt gaa ggt ggt Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu Thr Arg Glu Gly Gly 345 350 355				1698
tat cca aat gla ttt tac ggt gat tac tat ggg att cct aac gat aac Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Asn Asp Asn 360 365 370				1746

att tca gct aaa aaa gat atg att gat gag ctg ctt gat gca cgt caa 1794
 Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu Leu Asp Ala Arg Gln
 375 380 385

aat tac gca tat ggc acg cag cat gac tat ttt gat cat tgg gat gtt 1842
 Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His Trp Asp Val
 390 395 400 405

gta gga tgg act agg gaa gga tct tcc tcc aga cct aat tca ggc ctt 1890
 Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg Pro Asn Ser Gly Leu
 410 415 420

gcg act att atg tgc aat gga cct ggt ggt tcc aag tgg atg tat gta 1938
 Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser Lys Trp Met Tyr Val
 425 430 435

gga cgt cag aat gca gga caa aca tgg aca gat tta act ggt aat aac 1986
 Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp Leu Thr Gly Asn Asn
 440 445 450

gga gcg tcc gtt aca att aat ggc gat gga tgg ggc gaa ttc ttt acg 2034
 Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp Gly Glu Phe Phe Thr
 455 460 465

aat gga gga tct gta tcc gtg tac gtg aac caa taacaaaaag ccttgagaag 2087
 Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
 470 475 480

ggattcctcc ctaactcaag gctttcttta tgcgcttag ctttacgctt ctacgacttt 2147

gaagcttggg gatccgtcga gacaaggtaa aggataaaac agcacaattc caagaaaaac 2207

acgatitaga acctaaaaag aacgaatttg aactaactca taaccgagag gtaaaaaaag 2267

aacgaagtcg agatcaggga atgagtttat aaaataaaaa aagcacctga aaaggtgtct 2327

ttttitgatg tctaga 2343

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 1 5 10 15

Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
 20 25 30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
 85 90 95

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
 100 105 110
 Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
 115 120 125
 Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
 130 135 140
 Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
 145 150 155 160
 Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
 165 170 175
 Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
 180 185 190
 Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
 195 200 205
 Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
 210 215 220
 Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
 225 230 235 240
 Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
 245 250 255
 Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
 260 265 270
 Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
 275 280 285
 Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
 290 295 300
 Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
 305 310 315 320
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
 325 330 335
 Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
 340 345 350
 Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
 355 360 365
 Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
 370 375 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385 390 395 400

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
435 440 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
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Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
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ataatggtat ccaaattccac gc 22

<210> 40
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gttatccgct cacaattcat tcagtcatat gtatcacc 38

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<400> 41
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taatggagga gagaaggccg 20

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<400> 50
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